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## **Lipoxygenase overexpression in plants and reduction in plant sensitivity to diseases and to attacks from pathogenic organisms**

The present invention relates to methods for reducing plant sensitivity to diseases and attacks from pathogenic organisms. The methods according to the invention consist in overexpressing a lipoxygenase in plants so as to reduce their sensitivity to diseases and attacks. The invention also relates to expression cassettes, to vectors and to transformed plants used in the methods according to the invention.

Lipoxygenases (LOXs) are ubiquitous enzymes in higher plants and mammals. They catalyze the dioxygenation of polyunsaturated fatty acids containing a (Z,Z)-1,4-pentadiene unit. In plants, substrates for the enzyme are linoleic acid (C18:2) and linolenic acid (C18:3), which are two major constituents of cell membranes. These polyunsaturated fatty acids are generally complexed in the form of membrane-bound phosphoglycerolipids and are only accessible to LOXs after the action of a phospholipase type A<sub>2</sub> or lipolytic acyl hydrolases. Recent studies suggest, however, that certain LOXs may, under certain circumstances, oxidize esterified fatty acids and membrane-bound lipids (1-4). Arachidonic acid, which is not detectable in plants, but which is part of the membrane-bound constituents in oomycetes, is also a substrate for plant LOXs (5).

LOXs are classified according to the position of the carbon onto which the molecular oxygen is preferentially inserted. In plants, 13-LOXs and 9-LOXs are distinguished; the same enzyme can, however, use one or other position, indifferently or else with a preference for a position. This specificity can be modified according to the conditions of pH and of O<sub>2</sub> concentration of the medium (4). The position specificity of a LOX cannot be directly predicted according to its primary sequence, even though some structural elements related to this property are now known (6, 7).

The products formed in the reaction are fatty acid hydroperoxides, which are very reactive and capable of causing, via free-radical reactions, degradation of the major constituents of the cell (lipids, proteins, nucleic acids) (8). Fatty acid hydroperoxides are rapidly converted into a series of compounds having diverse biological activities. All the products derived from polyunsaturated fatty acids via oxygenation are collectively referred to as oxylipins.

Plant LOXs have been associated with varied physiological processes, on the basis of profiles of gene expression and of enzyme activity. Thus, it has been proposed that LOXs are involved in regulating seed maturation, germination, fruit maturation, and leaf and

flower senescence. The precise contribution of LOXs to these processes remains to be determined however. An important role is also attributed to LOXs in response to stress, in particular injury, and parasitic attacks (4, 5, 9). Strong induction of LOX gene expression is thus measured in many monocotyledon or dicotyledon plants when they interact with  
 5 bacteria, viruses or fungi, and also after mechanical injury or injury caused by insects on the leaves.

This diversity in the biological functions may be provided due to the presence of various isoenzymes, exhibiting very varied mechanisms of regulation and tissue and subcellular locations, according to the species and isoforms under consideration (5). Added  
 10 to this is the diversity of the oxylipins generated from the products of the LOX, which is modulated according to the type of hydroperoxide formed and to the nature of the enzymes which metabolize them.

The fatty acid hydroperoxides generated by the LOX are in fact converted according to several distinct enzyme pathways (4). The hydroperoxide lyase (HPL) pathway catalyzes  
 15 cleavage of 13- or 9-hydroperoxides of fatty acids so as to achieve the synthesis of volatile C6- or C9-aldehydes and of C12 or C9 short-chain acids, such as 12-oxo-*trans*-9-dodecenoic acid, the precursor of traumatic acid. C6-aldehydes play an important role in plant fragrance, but some, such as *trans*-2-hexenal, also have antimicrobial properties (10). It has recently been shown that *trans*-2-hexenal can act as a signal molecule for defense  
 20 gene activation (11). Traumatic acid, also referred to as wound hormone, is thought to have a role in tissue healing by promoting cell division at sites of injury (5).

A second enzyme pathway involved in the metabolism of fatty acid hydroperoxides produced by LOX concerns allene oxide synthase (AOS). This enzyme catalyzes the dehydration of 13-hydroperoxilinolenic acid and forms an allene oxide, which is the  
 25 precursor of the jasmonic acid. Jasmonic acid is a key molecule of plant signaling mechanisms for activating many defense genes (12), among which are the genes encoding protease inhibitors active against insects, and also many PR proteins (chitinase, defensin, thionin, glucanase). The role of jasmonates as a signal molecule has recently been underlined by various experiments showing that *Arabidopsis* mutants or tomato mutants  
 30 affected in terms of the biosynthesis of these molecules or the distinction thereof, exhibit a deficiency in defense gene induction (13), greater sensitivity to organisms which are normally nonpathogenic for wild-type plants (14) or reduced resistance to insects (15). A third enzyme pathway for conversion of hydroperoxides concerns the formation of divinyl ether fatty acids. These compounds, which can be formed from 13- or 9-hydroperoxides,

have been isolated from various plants. The first divinyl ether synthase (DES) was recently cloned in the tomato (16). The divinyl ether fatty acids produced from 9-hydroperoxides, colneleic acid and colnelenic acid, exhibit antifungal properties, in particular with respect to *Phytophthora infestans* (17).

5        Other modifications of the products of the reaction catalyzed by LOX concern epoxidations with epoxygenases and peroxygenases. This metabolic pathway allows the synthesis of molecules with antimicrobial activity and may be involved in the synthesis of cutin monomers, which, besides their structural function, can also induce the activity of defense genes (18).

10        The fatty acid hydroperoxides produced by LOX can, finally, generate the formation of free radicals involved in membrane degradation mechanisms associated with cell death (5).

      All these data therefore show that the initial activity of LOX is essential for the synthesis of a set of molecules, some of which exhibit antimicrobial activities or are  
15 involved in the signaling leading to defense.

      LOX activity increases notably in tobacco in response to elicitors (19, 20). The isolation of a LOX complementary DNA clone, in particular pTL-J2 (21), has made it possible to characterize the corresponding tobacco gene, called *LOX1*. DNA/RNA hybridization experiments (Northern hybridization) have shown that *LOX1* is expressed in  
20 tobacco cells in culture subsequent to the application of elicitor and in tobacco plants inoculated with the oomycete *Phytophthora parasitica nicotianae*, *Ppn* (22). The transcripts corresponding to this gene are not detectable in normal plants or untreated cells. A biochemical study shows that, *in vitro*, the LOX of elicited tobacco cells allows the production of 9- and 13-hydroperoxides of fatty acid, with preferential insertion of the  
25 molecular oxygen in the 9-position (20).

      Subsequent to root inoculation of tobacco with *Ppn*, strong induction of expression of the gene is measured. In the case of an incompatible interaction (resistant plant/avirulent race of microorganism), early induction of the activity of the gene is measured, with a maximum accumulation of transcripts at 24 hours (22). Induction of the gene is later and  
30 smaller in amplitude in the case of a compatible interaction (sensitive plant/virulent race), as has also been observed in other gene-for-gene models, such as interactions between the tomato and *Pseudomonas syringae* (23), rice and *Magnaporthe grisea* (24), and the potato and *Phytophthora infestans* (25). Expression of the *LOX1* gene is not detected in the tissues of normal tobacco plants, with the exception of flowering plants for which the LOX

transcripts are detected in low amount in the petals and sepals, and young germinations (22, 26). In the latter case, transient expression of the *LOX1* gene is detected between the second and fourth days after the beginning of germination.

Villalba et al. (27) have shown that an elicitor glycoprotein isolated from *Ppn* walls, called CBEL for Cellulose Binding Elicitor Lectin, induces the *LOX1* gene when it is infiltrated into the foliar mesophyll of tobacco plants. The *LOX1* transcripts appear during the first four hours following infiltration and reach a maximum level at 12 hours. A polysaccharide derived from marine algae,  $\lambda$ -carraghenan, also induces the *LOX1* gene when it is applied to tobacco plants by infiltration into the foliar mesophyll (28).

In tobacco cells, expression of the *LOX1* gene is detected subsequent to eliciting treatments. In the case of *Ppn* elicitor (wall extract), induction of expression of the *LOX1* gene is detected within the first two hours after treatment, with a maximum accumulation at 24 hours (22). Cryptogein, an elicitor peptide of *Phytophthora cryptogea*, an oomycete for which tobacco is not a host, and *Colletotrichum lindemuthianum* endopolygalacturonase, also make it possible to induce the *LOX1* gene (26). It has been shown, moreover, that induction of the *LOX1* gene occurs earlier than that of defense genes such as those encoding PR proteins, namely chitinases and  $\beta$ 1-3-glucanases, suggesting that the LOX pathway has a potential role in the signal transduction triggering the defense reactions (26). *LOX1* expression in cells is also inducible with methyl jasmonate (22, 29), thus indicating possible self-amplification of this pathway, whereas no accumulation of LOX transcripts is detected after the application of salicylic acid (22).

Analysis of expression of the *LOX1* gene shows that the induction of LOX constitutes an early response of the plant to infection with *Ppn*, suggesting a role in the establishment of resistance. This potential role has been confirmed through obtaining transgenic plants expressing the complementary DNA of the gene in an antisense orientation. In fact, these plants, originating from the 46-8 line normally resistant to *Ppn* race 0, exhibit greatly reduced levels of LOX activity and have lost their ability to trigger the incompatible reaction (30, 31). This experiment clearly shows that expression of the LOX gene is necessary to establish the resistant state in the gene-for-gene interaction between tobacco and *Ppn*. The LOX antisense plants are also more sensitive to another pathogenic fungus of tobacco, *Rhizoctonia solani* (30, 31). In parallel, Rust rucci et al. (32) have shown that 9-hydroperoxides accumulate during the hypersensitive-type response of tobacco to cryptogein, and that this accumulation is necessary for the development of this reaction. In another Solanacea, the potato, oxylipins derived from the 9-LOX pathway, in

particular colneleic acid and colnelenic acid, preferentially accumulate in cells in culture in response to a *P. infestans* elicitor (33). All these data suggest a major role for the 9-LOX pathway in Solanaceae, including tobacco, in the response to pathogenic agents, in particular oomycetes. In these plants, the 13-LOX pathway contributes to the response to pathogenic agents, as shown by the early synthesis of jasmonates (29); it is also involved in the response to injury and to insects. Thus, potato plants expressing a 13-LOX antisense construct have been found to be more sensitive to insect attack (34).

Few attempts at overexpressing a LOX in plants have been reported in the literature. In fact, the expression of a LOX poses questions of feasibility due to the potentially toxic properties of LOXs, if they directly oxidize biomembranes, and of the products which they form.

In tobacco, introduction of soybean LOX2 under the control of a chimeric promoter, formed by fusion of the cauliflower mosaic virus (CaMV) 35S promoter and an enhancer isolated from the alfalfa mosaic virus, has made it possible to produce transgenic calluses exhibiting a LOX activity which is approximately 2 times greater than that of calluses transformed with the vector lacking LOX sequence. These calluses are capable of forming 3 to 6 times as many volatile aldehydes, products of the 13-LOX pathway via a 13-HPL, as the control calluses. Transgenic plants were regenerated from these calluses but, although these plants exhibited a high accumulation of the heterologous protein, their LOX activity is no different from that of control plants. However, they form larger amounts of volatile aldehydes than control plants (35). More recently, a 13-LOX specific for the lipid bodies of cucumber seeds has been expressed in tobacco (36). The heterologous protein accumulates throughout the plant, in transgenic tobacco plants, and in particular in the seeds, where it is essentially located in the lipid bodies as in the cucumber. Its presence results in a qualitative modification of the LOX activity of the transgenic plants, both *in vitro* and *in vivo*. An *Arabidopsis* chloroplast 13-LOX, AtLOX2, has been used in a construct in the sense orientation, under the control of the CaMV 35S promoter, to transform garden arabis plants. The authors focus, however, on the transformation events which led to a decrease in LOX activity by cosuppression (37). Finally, in the lentil, transient transformation of protoplasts with a construct containing a lentil LOX under the control of the CaMV 35S promoter produced a 20% increase in the LOX activity of these protoplasts (38). None of the transformed plants or cultures described above was tested with respect to a response relating to attack from pathogenic agents. Moreover, the experiments carried out essentially concern 13-LOXs.

In addition, the hypotheses concerning the participation of lipoxygenases in plant defense mechanisms are essentially based on the biological activities of certain oxylipins (39). Now, the biosynthesis of most oxylipins, and in particular jasmonic acid and the volatile aldehydes derived from the 13-LOX pathway, and the divinyl ethers derived from the 9-LOX pathway, requires the activity of enzymes which metabolize the LOX products, such as AOS, HPL or DES, beyond the LOX itself. Expression of the genes corresponding to these enzymes is often inducible. In the tomato and *Arabidopsis thaliana*, the expression genes encoding AOS and HPL is wound-inducible (40-42). Consequently, the action of only lipoxygenases does not therefore appear to be sufficient to trigger plant resistance mechanisms.

Cultivated plants are subjected to attack by many pathogenic organisms, such as viruses, bacteria and fungi, but also pests such as insects. These attacks weaken the plants and decrease their crop yields. There is therefore a considerable need to increase the resistance mechanisms of plants and to decrease their sensitivity to diseases and attacks from parasitic or pathogenic organisms. The mechanisms of responsive plants to attacks from pathogenic agents have been the subject of many studies. It is now commonly accepted that the lipoxygenase pathway in plants contributes to their system of defense and to establishing a state of resistance through the oxylipin pathway in particular.

However, knowledge of these metabolic pathways and of the lipoxygenases has not made it possible to develop methods for directly increasing plant resistance.

This problem is solved by the present invention since it has now been noted that overexpression of a lipoxygenase in plants directly reduces plant sensitivity to diseases and attacks from pathogenic agents. Unexpectedly, and although lipoxygenase is part of complex metabolic pathways, overexpression of a lipoxygenase in plants is sufficient to improve plant response to attacks from pathogens. In addition, overexpression of the lipoxygenase does not substantially affect the phenotype of the transformed plants, besides the novel acquired properties.

The present invention therefore consists in overexpressing a lipoxygenase in plants so as to reduce plant sensitivity to diseases and attacks from pathogenic organisms or pests. A subject of the invention is also preferred expression cassettes for overexpressing the lipoxygenase in plants, and also plant cells and transformed plants.

### **Description of the sequence listing**

- SEQ ID No. 1: Tobacco lipoxygenase (LOX1).  
 SEQ ID No. 2: CaMV 35S promoter – coding sequence of tobacco *LOX1* gene – nos terminator expression cassette.  
 5 SEQ ID Nos. 3-6: Primers for PCR.

### **Description of the invention**

The present invention relates to a method for reducing plant sensitivity to diseases  
 10 and attacks from pathogenic organisms. This method consists in overexpressing a lipoxygenase in these plants.

The term "lipoxygenase" means an enzyme which catalyzes the dioxygenation of polyunsaturated fatty acids containing a (Z,Z)-1,4-pentadiene unit. In plants, the substrates for the enzyme are linoleic acid (C18:2) and linolenic acid (C18:3), which are two main  
 15 constituents of cell membranes.

The term "overexpression" means that the lipoxygenase is expressed at a level greater than the expression level observed in a reference plant (not induced). This overexpression results in greater accumulation of the lipoxygenase gene transcripts and of the lipoxygenase itself, and in an increased lipoxygenase specific activity in the tissues of  
 20 the plant. To reduce plant sensitivity to diseases and attacks from pathogenic organisms, it is important for the level of expression of the lipoxygenase to be greater than that of a reference plant when the attack on the pathogenic organism occurs.

Overexpression of the lipoxygenase makes it possible to reduce plant sensitivity to disease and attacks from pathogenic organisms. The expression "attack from pathogenic  
 25 organisms" is in particular attacks on the plants from viruses, bacteria, fungi, oomycetes or insects.

In a preferred embodiment, the method consists in constitutively overexpressing a lipoxygenase in plants. The term "constitutively" denotes temporal and spatial expression of the lipoxygenase in plants in the methods according to the invention. The term  
 30 "constitutively" means the expression of a lipoxygenase in the tissues of the plant throughout the life of the plant and in particular during its entire vegetative cycle. In a first embodiment, the lipoxygenase is expressed constitutively in all plant tissues. In a second embodiment, the lipoxygenase is expressed constitutively in the roots, the leaves, the stems,



the flowers and/or the fruits. In another embodiment of the invention, the lipoxygenase is expressed constitutively in the roots, the leaves and/or the stems.

In a particular embodiment of the invention, the lipoxygenase is a lipoxygenase which is "inducible" in a reference plant. In the present invention, lipoxygenase which is  
5 "inducible" means a lipoxygenase which is not expressed, or is expressed at very low levels, and the expression of which is greatly induced in response to elicitors in the response to stress, to wounds, and in particular to diseases and attacks from pathogenic organisms.

In a preferred embodiment of the method according to the invention, the lipoxygenase preferably has 9-lipoxygenase activity. Lipoxygenases (LOX) are classified  
10 according to the position of the carbon onto which the molecular oxygen is preferentially inserted. In plants, 13-LOXs and 9-LOXs are distinguished. Methods for determining the specificity of lipoxygenase activity are described in the literature (Fournier et al., *Plant J.* 3:63-70, 1993; Hornung et al., *PNAS* 96:4192-4197, 1999; Rustérucchi et al., *J. Biol. Biochem.* 274:36446-36455, 1999).

15 Any lipoxygenase the overexpression of which in plants makes it possible to reduce plant sensitivity to diseases and attacks by pathogen organisms can be used in the methods according to the invention. Lipoxygenases are known to those skilled in the art, and other lipoxygenases can be identified using known techniques. By way of example, mention may in particular be made of potato (Kolomoiets M.V. et al., *Plant Physiol.* 124:1121-1130,  
20 2000), tomato (Genbank AY008278) and potato tuber (Royo et al., *J. Biol. Chem.*, 271:21012-21019, 1996; Casey, R., *Plant Physiol.*, 107:265-266, 1995), lipoxygenases, almond seed lipoxygenase (Mita et al., *Eur. J. Biochem.*, 268:1500-1507, 2001) and barley seed lipoxygenase (Van Mechelem et al., *Biochem. Biophys. Acta*, 1254:221-225, 1995).

The lipoxygenase is preferably a plant lipoxygenase.

25 In a particular embodiment of the invention, it is a Solanacea plant lipoxygenase. Among the Solanacea plants, mention may in particular be made of tobacco, tomato, potato or else pepper.

In another preferred embodiment of the invention, the lipoxygenase exhibits at least 80% homology with the tobacco lipoxygenase 1 (LOX1) of SEQ ID No. 1. Advantageously,  
30 the percentage homology will be at least 80%, 85%, 90%, 95%, and preferably at least 98%, and more preferably at least 99%, with respect to SEQ ID No. 1. The term "homolog" denotes a polypeptide which may exhibit a deletion, an addition or a substitution of at least one amino acid. The methods for measuring and identifying homologies between polypeptides or proteins are known to those skilled in the art. Use may, for example, be

made of the UWGCG package and the BESTFIT program for calculating homologies (Devereux et al., *Nucleic Acid Res.* 12, 387-395, 1984). Preferably, the homologous lipoxigenases conserve the same biological activity as the tobacco lipoxigenase (LOX1) of SEQ ID No. 1. Preferably, these polypeptides therefore have a lipoxigenase activity, and  
5 even more preferably 9-lipoxigenase activity.

In an even more preferred embodiment, the methods according to the present invention use the lipoxigenase of SEQ ID No. 1.

Overexpression of the lipoxigenase in plants is carried out by transforming the plants with, or by applying to the plants, a molecule for stimulating lipoxigenase synthesis  
10 in the plant.

In a preferred embodiment of the invention, the lipoxigenase is overexpressed by integration into the genome of the plants of an expression cassette comprising a sequence encoding a lipoxigenase under the control of a promoter which is functional in plants.

According to the invention, the term "promoter" means the noncoding region of a  
15 gene involved in binding the RNA polymerase and with other factors which are responsible for initiating and regulating transcription leading to the production of an RNA transcript. The plant promoters which can be used in the methods according to the present invention are widely described in the literature.

The promoter is preferably a promoter which is constitutive in plants. The  
20 constitutive promoters which can be used in the method according to the invention are also well known to those skilled in the art.

As a promoter regulatory sequence in plants, use may be made of any promoter sequence for a gene which is naturally expressed in plants, such as, for example, "constitutive" promoters of bacterial, viral or plant origin. Mention may be made of  
25 bacterial promoters such as that of the octopine synthase gene or of the nopaline synthase gene, viral promoters, such as the cauliflower mosaic virus 35S promoter or the CSVMV promoter (WO 97/48819), and promoters of plant origin such as the histone gene promoter (EP0507698) or the promoter of a rice actin gene (US 5,641,876). According to the invention, use may in particular be made, in combination with the promoter regulatory  
30 sequence, of other regulatory sequences, which are located between the promoter and the coding sequence, such as transcription activators (enhancers).

In a preferred embodiment of the invention, the constitutive promoter is the cauliflower mosaic virus 35S promoter.

In another embodiment of the invention, the constitutive expression or the overexpression of the lipoxygenase is obtained by transforming the plants so as to place a constitutive promoter or an enhancer sequence upstream of or in the vicinity of the lipoxygenase gene in the plants. Use may in particular be made of any regulative sequence  
5 for increasing the level of expression of lipoxygenase in plants.

Preferably, the lipoxygenase is overexpressed in the stems, the leaves and/or the roots of the plant.

According to the invention, the term "plant" means any differentiated multicellular organism capable of photosynthesis, in particular monocotyledons or dicotyledons, more  
10 particularly crop plants which may or may not be intended for animal or human food, such as maize, wheat, barley, sorghum, rapeseed, soybean, rice, cane sugar, beetroot, tobacco, cotton, etc.

Overexpression of the lipoxygenase can be obtained in any plant according to methods known to those skilled in the art.

15 In a particular embodiment of the invention, the plants are chosen from Solanaceae plants. Among the Solanaceae plants mention will in particular be made of tobacco, tomato, potato or else pepper.

In a preferred embodiment of the invention, the lipoxygenase is overexpressed by integration into the plant genome of an expression cassette comprising a sequence encoding  
20 a lipoxygenase under the control of a promoter which is functional in plants. A polynucleotide encoding a lipoxygenase is inserted into an expression cassette using cloning techniques well known to those skilled in the art. This expression cassette comprises the elements required for transcription and translation of the sequences encoding the lipoxygenase in plants. Advantageously, this expression cassette comprises both elements  
25 for making the transformed plants produce the lipoxygenase and elements required for regulating this expression. The present invention also relates to preferred expression cassettes which can be used in the methods according to the invention.

In one embodiment, the present invention relates to expression cassettes which are functional in plant cells and plants, comprising a promoter having constitutive activity in  
30 plants, controlling the expression of a polynucleotide encoding a lipoxygenase at least 90% homologous to the lipoxygenase of SEQ ID No. 1. Advantageously, the percentage homology will be at least 80%, 85%, 90%, 95%, and preferably at least 98%, and more preferably at least 99%, with respect to SEQ ID No. 1. Preferably, this polynucleotide encodes a lipoxygenase having 9-lipoxygenase activity. More preferably, this

polynucleotide encodes the lipoxygenase of SEQ ID No. 1. In a particular embodiment of the invention, the promoter is the cauliflower mosaic virus 35S promoter.

The expression cassettes according to the invention preferably comprise a terminator sequence. These sequences allow termination of transcription and polyadenylation of the mRNA. Any terminator sequences which is functional in plants can be used. For expression in plants, use may in particular be made of the *Agrobacterium tumefaciens nos* terminator, or else terminator sequences of plant origin, such as, for example, the histone terminator (EP 0 633 317), the CaMV 35S terminator or the *tml* terminator. The terminator sequences can be used in monocotyledon and dicotyledon plants.

10 The techniques for construction of these expression cassettes are widely described in the literature (see in particular Sambrook et al., Molecular Cloning : A Laboratory Manual, 1989).

Advantageously, the expression cassettes according to the present invention are inserted into a vector for replicating them or for transforming plants.

15 The present invention also relates to vectors for transforming plants, comprising at least one expression cassette according to the present invention. This vector may in particular consist of a plasmid or of a virus into which is inserted an expression cassette according to the invention. Many vectors have been developed for transforming plants with *Agrobacterium tumefaciens*. Other vectors are used for transformation techniques not based on the use of *Agrobacterium*. These vectors are well known to those skilled in the art and widely described in the literature. Preferably, the vectors of the invention also comprise at least one selection marker. Among the selection markers, mention may be made of genes for resistance to antibiotics, such as the *nptII* gene for kanamycin resistance (Bevan et al., Nature 304:184-187, 1983) and the *hph* gene for hygromycin resistance (Gritz et al., Gene 25:179-188, 1983). Mention will also be made of genes for tolerance to herbicides, such as the *bar* gene (White et al., NAR 18:1062, 1990) for tolerance to bialaphos, the EPSPS gene (US 5,188,642) for tolerance to glyphosate or else the HPPD gene (WO 96/38567) for tolerance to isoxazoles.

The present invention also relates to vectors comprising an expression cassette according to the invention.

A subject of the invention is also a method for transforming plants with an expression cassette or a vector according to the invention.

According to the present invention, the plant transformation can be obtained by any suitable known means; plant transformation techniques are fully described in the specialist literature.

Certain techniques use *Agrobacterium* in particular for transforming dicotyledons. A series of methods consists in using a chimeric gene inserted into an *Agrobacterium tumefaciens* Ti plasmid or an *Agrobacterium rhizogenes* Ri plasmid as means of transfer into the plant. Other methods consist in bombarding the cells, protoplasts or tissues with particles to which the DNA sequences are attached. Other methods can also be used, such as microinjection or electroporation, or else direct precipitation with PEG.

Those skilled in the art will soon see appropriate methods as a function of the nature of the plant cell or of the plant.

The present invention relates to the transformed plant cells comprising an expression cassette and/or a vector according to the invention.

According to the invention, the term "plant cell" means any cell derived from a plant and which can constitute undifferentiated tissues such as calluses, differentiated tissues such as embryos, parts of plants, plants or seeds.

The present invention also relates to the transformed plants comprising an expression cassette, a vector and/or transformed cells according to the invention.

According to the invention, the term "plant" means any differentiated multicellular organism capable of photosynthesis, in particular monocotyledons or dicotyledons, more particularly crop plants which may or may not be intended for animal or human food, such as maize, wheat, barley, sorghum, rapeseed, soybean, rice, beetroot, tobacco, cotton, etc.

## **FIGURES**

25

**Figure 1** Figure 1 presents the construct 35S-9-LOX used to transform tobacco. The 9-LOX (*LOX1*) coding sequence was obtained by PCR amplification and then inserted between the cauliflower mosaic virus 35S promoter (35S) and the *Agrobacterium tumefaciens* nopaline synthase terminator (tnos). This vector also comprises the neomycin phosphotransferase (*NPTII*) gene which confers resistance to kanamycin in bacteria and plants. "F" ("sense 35S") denotes the sense primer and "R" ("reverse LOX1") denotes the reverse primer.

30

**Figure 2**

Figure 2 is a histogram representing the measurement of LOX specific activity in the tobacco plant stems in nKAT/mg of protein. 46-8 WT and 49-10 WT denote the parental lines. S46-21, S46-26 and S49-18 denote the transgenic lines. In fact, prior to *Ppn* inoculation tests, the LOX specific activity and also the level of corresponding transcripts were analyzed for 12-week-old tobacco plant stems. It is observed that the level of LOX specific activity in the three transgenic lines selected is significantly higher than that measured in the corresponding parental lines.

**Figure 3**

Figure 3 is a histogram representing the measurement of lesion length in mm. These measurements were made 48 hours (48h) or 72 hours (72h) after inoculation. The numbers in brackets correspond to the independent repetitions carried out. The two lines S46-21 and S46-26, inoculated with *Ppn* 1, exhibit lesion length significantly shorter than those obtained with the same pathogenic agent in the wild-type parent, 46-8 WT. Similarly, the line S49-18 exhibits shorter lesions than those measured in its wild-type parent, 49-10 WT, when these two lines are inoculated with *Ppn* 0. These differences are significant at 48 hours and at 72 hours after inoculation.

**EXAMPLES****Example 1: Biological material**

Wild-type tobacco plants (*Nicotiana tabacum* L.) of the two near-isogenic lines 46-8 (46-8 WT) and 49-10 (49-10 WT) were used (Helgeson et al., *Phytopath.* 62,1439-1443, 1972). These lines differ from one another by the presence, in the 46-8 WT line, of a locus for resistance to race 0 of *Ppn*. Thus, the 46-8 WT line is resistant to race 0 of *Ppn* and sensitive to race 1 of this pathogenic agent, whereas the 49-10 WT line is sensitive to the two races of *Ppn*.

The seeds of wild-type or transgenic lines are sterilized (Rancé et al., *Plant Cell Report*, 13, 647-651, 1994) and sown on solid MS medium supplemented, in the case of the transgenic lines, with kanamycin (50  $\mu\text{g}.\text{ml}^{-1}$ ). After 4 weeks of growth *in vitro* (40% hygrometry, constant temperature 25°C, light 60  $\mu\text{mol}.\text{m}^{-2}.\text{s}^{-1}$ : 16h, dark: 8h), the kanamycin-resistant wild-type or transgenic plants are transferred onto vermiculite in a culture room (80% hygrometry, light 125  $\mu\text{mol}.\text{m}^{-2}.\text{s}^{-1}$ : 16h, 25°C, dark: 8h, 18°C).

The *Ppn* strains used correspond to the 1156 (race 0) and 1452 (race 1) isolates (Hendrix, J.W. & Apple, J.L., *Tobacco Science* 11, 148-150, 1967). The *Ppn* mycelium is cultured in the dark on a solid synthetic medium (Keen, N.T., *Science* 187, 74-75, 1975).

5 **Example 2: Production of the CaMV 35S promoter-LOX1 coding sequence-nos terminator cassette (p35S-LOX1)**

TL-J2 is a 2888 bp complementary DNA corresponding to the tobacco *LOX1* gene induced by pathogenesis. The production of this complementary DNA is described by Véronési et al. (Véronési et al., *Plant Physiol.* 108, 1342, 1995), and its sequence is  
 10 deposited in GenBank under the accession number X84040. This cDNA was used as a matrix for PCR amplification of the *LOX1* coding sequence.

Primers were synthesized to amplify a 2.6 kb DNA fragment covering positions 49 to 2667 of the cDNA:

- Sense primer = 5'-GTTATCAAACAGTTTAAAATGTTTCTGGAG-3'
- 15 - Reverse primer = 5'-TGATTTAAAGTTCTATATTGAC-3'

These primers enable, in addition, the introduction of *DraI* sites (underlined in the primer sequence) upstream of the translation initiation: and downstream of the stop codon (indicated in bold characters in the primer sequence) of the *LOX1* sequence.

The PCR reaction was carried out in a total volume of 25  $\mu$ l, containing 50 ng of  
 20 plasmid pTL-J2, 50 pmol of each of the sense and reverse primers above and 2.5 units of *Pfu* DNA polymerase (Stratagene Cloning Systems), and adjusted to 200  $\mu$ M of each dNTP and 2 mM  $MgCl_2$ . After denaturation for 5 min at 94°C, the thermocycler program was made up of 20 cycles, each including denaturation for 1 min at 94°C, hybridization for 1 min at 50°C and extension for 6 min at 72°C, followed by a final step of extension for  
 25 40 min at 72°C.

The DNA from this reaction was digested with *DraI* and separated on 0.8% agarose gel. The 2.6 kb blunt-ended fragment was purified from the gel (QiaEx II kit, Qiagen) and cloned into the *SmaI* site of the vector pIPM0 (Rancé et al., *PNAS* 6554-6559, 1998) between the CaMV 35S promoter and the 3' untranslated region of the *Agrobacterium*  
 30 *tumefaciens* nopaline synthase gene (nos terminator). This vector also comprises two copies of the neomycin phosphotransferase (*NPTII*) gene which confers kanamycin resistance in bacteria and plants. The ligation mixture was used to transform competent *Escherichia coli* XL1 Blue bacteria, and kanamycin-resistant colonies were selected and then screened for the presence of LOX sequence using the TL-J2 molecular probe. Positive colonies were

cultured and the corresponding plasmids were purified. The orientation of the LOX1 sequence was examined for each of the plasmids by PCR using the following primers:

- F primer, “sense 35S”: 5’-GGCCATGGAGTCAAAGATTC-3’ targeting nucleotide 6906-6925 of the CaMV 35S promoter (sequence available in Genbank under the accession number J02048).
- R primer, “reverse *LOX1*”: 5’-GCTCTGGCATGAAATTTTCG-3’ targeting nucleotides 2290-2272 (noncoding strand) of TL-J2.

The amplification reactions were carried out in the volume of 50  $\mu$ l and comprising 100 ng of test plasmid, 10 pmol of each primer and 1 unit of *Taq* DNA polymerase in a medium adjusted to 200  $\mu$ M of each dNTP and 1.5 mM  $MgCl_2$ . The thermocycler program included an initial denaturation step of 5 min at 94°C, and then 40 cycles each consisting of denaturation for 1 min at 94°C, hybridization for 1 min at 65°C and extension for 2 min at 72°C, followed by a final elongation step for 10 min at 72°C. The reaction products were separated on 0.8% agarose gel. A plasmid for which the presence of an amplification product of the expected size (2.8 kb) indicated the sense orientation of the LOX sequence relative to the CaMV 35S promoter in the construct was selected. The LOX sequence and the junctions thereof with the promoter and the terminator were entirely sequenced. The plasmid thus verified is called p35S-*LOX1*. The sequence of the CaMV 35S-*LOX1* construct is described in SEQ ID No. 2.

### **Example 3: Genetic transformation of tobacco**

The plasmid p35S-*LOX1* was mobilized in the *Agrobacterium tumefaciens* strain LBA4404 by heat shock (Holsters et al., *Mol. Gen. Genet.* 163, 181-187, 1978). A kanamycin-resistant colony was isolated, the plasmid was purified, and the entire construct was verified by PCR with the F and R primers and under the conditions described above for determining the relative orientation of the LOX sequence. The recombinant bacteria obtained were then used to infect foliar discs of tobacco, *Nicotiana tabacum*, lines 46-8 WT and 49-10 WT, according to already described protocols (Horsch et al., *Science* 227, 1229-1231, 1985).

The plants regenerated on a Murashige and Skoog (MS) medium containing 150  $\mu$ g.ml<sup>-1</sup> of kanamycin were placed in a culture chamber and then in a greenhouse so as to obtain T1 seeds, by self-pollination. The transgenic lines regenerated from the parental lines 46-8 WT and 49-10 WT are called S46-x and S49-x plants, respectively.



#### **Example 4: Characterization of the primary transformants**

The presence of the 35S-*LOX1* expression cassette and also the number of copies of the transgene in the genome of the regenerated plants were determined by PCR and DNA/DNA (Southern) hybridization experiments. The genomic DNA of wild-type plants or  
 5 of regenerated plants which were resistant to kanamycin was prepared according to the method described by Dellaporta et al. (Dellaporta et al., *Plant Mol. Biol. Rep.* 1, 19-21, 1983). The entire T-DNA transferred was verified by PCR amplification using the F “sense 35S” and R “reverse *LOX1*” primers described above. The reaction conditions were those described above, but the amount of matrix DNA was, in this case, 800 ng of genomic DNA.  
 10 The number of copies of T-DNA inserted was estimated by Southern blotting (50). The genomic DNA (15 µg) was digested with *Bam*H1 and the digestion products were separated on agarose gel and then transferred onto nylon membrane. A CaMV 35S probe (nucleotides 6909 to 7440 of the Genbank sequence J02048) was used after labeling with [ $\alpha$ -<sup>32</sup>P] dCTP. The number of bands hybridizing this probe, after revelation by autoradiography, is a good  
 15 indication of the number of sites and insertion of the construct.

#### **Example 5: Transformation of tobacco with the sequence encoding tobacco *LOX1* under the control of the CaMV 35S constitutive promoter**

In order to constitutively express tobacco *LOX1* in transgenic tobacco plants, the  
 20 corresponding coding sequence was introduced in the sense orientation into the transfer DNA of the binary vector pIPM0, downstream of the CaMV 35S constitutive promoter (p35S) (Fig. 1A). This construct, called p35S-*LOX1*, also contains a kanamycin resistance gene (*NPTII*) for selecting the transformed plant cells. The 46-8 WT and 49-10 WT tobacco lines were transformed with *Agrobacterium tumefaciens* LBA 4404 into which the  
 25 p35S-*LOX1* construct has been introduced. 15 independent primary transformants S46-x derived from the 46-8 WT line were regenerated from calluses selected on a medium containing kanamycin. The letter x denotes the number of the plant obtained. Similarly, 25 independent primary transformants S49-x were regenerated from the 49-10 WT line. These plants were acclimatized in a culture chamber and then transferred into a greenhouse until  
 30 flowering. The seeds corresponding to the T1 plants were obtained by self-pollination of the primary transformants.

The entire construct introduced into the genome of the transgenic plants was verified by PCR amplification using a preparation of genomic DNA of the primary transformants cultured on kanamycin, and a pair of primers, one specific for the 5' region of the CaMV

35S promoter (F) and the other for the 3' region of the *LOX1* coding sequence (R). The amplification products were separated on agarose gel and revealed with ethidium bromide. For 10 of the 11 primary transformants analyzed, the profile obtained corresponds to a single band for which the size (2.8 kb) corresponds to the estimated size of the product. In addition, this profile is identical to that obtained with the binary vector p35S-*LOX1*, which suggests that at least one copy has been integrated into the genome of these transformants. On the other hand, one primary transformant does not have such a profile, although it is resistant to kanamycin, indicating an incomplete integration of the construct. The parental lines 46-8 WT and 49-10 WT, analyzed as negative controls, show no signal corresponding to the construct.

The number of copies inserted into each of the regenerated lines was estimated by Southern-type hybridization using genomic DNA digested with *Bam*HI and a probe homologous to the CaMV 35S promoter. The transfer DNA has two *Bam*HI sites: the first is located between the CaMV 35S promoter and the *LOX1* sequence and a second is located in the *LOX1* sequence. The *Bam*HI fragments which hybridize with the radiolabeled CaMV 35S probe therefore result from a first cleavage between the CaMV 35S promoter and *LOX1* and a second cleavage in the plant genome, upstream of the left border of the transfer DNA. Since the insertion of the transfer DNA into the plant genome is random, the *Bam*HI fragments which hybridize with the radiolabeled CaMV 35S probe, obtained in the case of multiple insertions, will have sizes which depend on the position of the *Bam*HI site in the genomic DNA and which are therefore probably different. For this reason, the number of these fragments makes it possible to evaluate the number of sites for insertion into the genome. The profiles obtained indicate that the primary transformants S46-3, S46-4, S46-26, S49-8 and S49-13 contain one copy of the transgene, whereas two copies have been inserted into the genome of the lines S49-18 and S49-28, and three copies into the genome of the lines S46-21, S49-14 and S49-30. The radiolabeled CaMV 35S probe did not hybridize with the genomic DNA corresponding to the S49-24 lines, or with that of the parental lines 46-8 WT and 49-10 WT.

### 30 **Example 6: RNA extraction and analysis**

The total RNA was isolated from frozen samples of T1 generation or wild-type plants. The plant material was ground in liquid nitrogen and the RNA was extracted using the Extract-all kit (Eurobio). The nucleic acid concentration was estimated by spectrophotometry. Northern blotting experiments were carried out as previously described

(Rickauer et al., *Planta* 202, 155-162, 1997). The filters were hybridized with the radiolabeled TL-J2 probe.

#### **Example 7: Analysis of LOX transcript accumulation in the T1 transgenic lines**

5        The level of LOX expression was evaluated in the various T1 transgenic lines by measuring the LOX transcript accumulation by Northern blotting. The total RNA samples were prepared from 4-week-old young transgenic tobacco plants selected *in vitro* on a medium containing kanamycin. Evaluation of the respective levels of expression of the transgene in the lines was carried out by comparing the obtained profiles with the level of  
10 transcripts detected in wild-type plants, and also in a control tobacco cell suspension (negative control) or in a suspension of tobacco cells treated with *Ppn* elicitors (positive control). The results obtained indicate that the level of transcripts is low, or even undetectable, in the transgenic lines S46-3, S46-4, S49-8, S49-13, S49-24, S49-28 and S49-30. On the other hand, the lines S46-21, S46-26, S49-14 and S49-18 exhibit a  
15 considerable accumulation of LOX transcripts, reaching, after quantification, from 30 to 66% of the level detected in the elicited tobacco cells. No LOX transcript accumulation is detected in the wild-type line or in the control tobacco cells. Introduction of the 35S promoter-*LOX1* construct into the tobacco plant is therefore accompanied by considerable constitutive expression in the transgenic lines S46-21, S46-26, S49-14 and S49-18.

20

#### **Example 8: Immunodetection of LOX**

Production of an anti-tobacco LOX1 rabbit polyclonal serum: Rabbits were immunized with a fusion protein expressed in *Escherichia coli* and comprising the 244 C-terminal residues of tobacco LOX1 fused with *Schistosoma japonicum* glutathione S-  
25 transferase (GST). An *XhoI* fragment of pTL-J2, corresponding to nucleotides 1921 to 2888, was inserted into the *XhoI* site of the vector pGEX-5X-3 (Pharmacia, sequence available in Genbank under the accession number U13858) which made it possible to obtain a translational fusion with the GST coding sequence. A colony of bacteria containing the recombinant plasmid was selected and placed in culture. These bacteria were treated with  
30 4 mM isopropylthio- $\beta$ -galactoside for 16 hours at 37°C in order to induce fusion protein production. The bacteria were harvested by centrifugation at 6000 x g for 10 min and the proteins were then extracted by resuspension of the bacterial pellet in a buffered solution adjusted to 140 mM NaCl, 2.7 mM KCl, 10 mM Na<sub>2</sub>HPO<sub>4</sub>, 1.8 mM KH<sub>2</sub>PO<sub>4</sub>, pH 7.3, in a proportion of 40  $\mu$ l of solution per ml of culture, and then sonication of the mixture in 3

cycles each of 1 min, on ice. The sonicate was centrifuged at 10 000 x g for 5 min and the insoluble proteins contained in the centrifugation pellet were recovered and extracted in 1X SDS-PAGE loading buffer (50) at 100°C for 10 min. After further centrifugation at 10 000 x g for 5 min, the protein extract was loaded onto an 8% polyacrylamide denaturing gel. After electrophoresis and restaining with Coomassie blue, the gel was destained and the band corresponding to the fusion protein (55 kDa) was excised from the gel and used to immunize the animals (Eurogentec). One of the sera, which exhibited the best titer relative to the fusion protein and to tobacco LOX1 was selected as anti-LOX1 serum. Western blotting analysis: Dialyzed and concentrated enzyme extracts, prepared as described above, were separated by SDS-PAGE on a 10% gel at a rate of 100 µg of protein per lane and, after electrophoresis, the separated proteins were transferred onto nitrocellulose membrane by electroblotting. The Western blotting analyses were carried out according to standard protocols. The anti-LOX1 serum, at a 1:1000 dilution, was used as primary antibody, and anti-rabbit IgG goat IgGs, coupled to alkaline phosphatase (sigma), were used as secondary antibodies. The alkaline phosphatase enzyme activity was detected by the NBT-BCIP method.

#### **Example 9: Detection of the LOX1 protein in the T1 transgenic lines**

Western blotting analysis was used to search for the *LOX1* protein in the transgenic lines constitutively expressing the LOX1 transgene. Soluble protein extracts prepared from the aerial parts of 8-week-old plants were separated by SDS-PAGE. The LOX1 protein was detected using a rabbit polyclonal serum directed against the C-terminal portion of the LOX1 protein. Immunochemical revelation shows the presence of a single band in the lanes corresponding to the transgenic lines S46-26 and S49-18. The size of the corresponding product, between 79 and 101 kDa, is coherent with the size calculated from the primary sequence of the LOX1 protein (92 kDa). On the other hand, the LOX1 protein is not detected in the extracts prepared from the parental lines 46-8 WT and 49-10 WT. Constitutive expression of the *LOX1* transgene is therefore accompanied by accumulation of the corresponding protein in the transgenic lines S46-26 and S49-18.

#### **Example 10: Measurement of the LOX activity**

The samples of wild-type or transgenic plants were frozen and then ground in liquid nitrogen and homogenized in 0.25 M sodium phosphate buffer, pH 6.5, containing 5% polyvinylpolypyrrolidone, at a rate of 1 ml of buffer per g of fresh material. After thawing,

the extracts were mixed by vortexing and centrifuged for 5 min at 12 000 x g. The centrifugation supernatant constitutes the crude enzyme extract. Two methods for measuring the LOX activity were used.

**Chromatographic method (TLC):** A protocol was adapted from a method described by Caldelari and Farmer (Caldelari, D. & Farmer, E.E., *Phytochemistry* 47, 599-604, 1998). The LOX assay was carried out with an aliquot of the crude enzyme extract corresponding to 50 µg of proteins, in a total volume of 0.4 ml of 0.25 M sodium phosphate buffer, pH 6.5, saturated with air and containing linoleic acid labeled with  $^{14}\text{C}$  on the carbon in the 1-position, at a final concentration of 1.2 µM, for 30 min at 30°C. The reaction mixture was then extracted twice with a methanol/chloroform (2:1) mixture and the organic phases were concentrated under a stream of nitrogen. The extracts were separated by thin layer chromatography on silica plates, in an ether/hexane/formic acid (70:30:1) mixture. The radiolabel products derived from metabolization of the linoleic acid and also the remaining substrate were revealed by phosphorimaging. The amount of substrate remaining in each reaction was estimated by comparison with a control reaction without enzyme extract (ImageQuaNT<sup>®</sup> software)

**Spectrophotometric method:** The crude enzyme extract was dialyzed and concentrated by centrifugation on an Ultrafree-4 unit (millipore) equipped with a Biomax 10 kDa NMWL membrane, for 30 min at 3500 x g and at 4°C, and was then subjected to three washing steps by addition of 0.5 ml of 0.25 M sodium phosphate buffer, pH 6.5 and centrifugation in the same unit. The LOX activity was determined in an assay consisting of a total volume of 475 µl, by measuring the formation of conjugated dienes at  $\lambda_{234}$  nm ( $\epsilon = 27\,000\text{ M}^{-1}\cdot\text{cm}^{-1}$ ) for 4 min at 30°C, in air-saturated 0.25 M sodium phosphate buffer, pH 6.5. The linoleic acid was used as substrate at a final concentration of 820 µM. The results are expressed in nanokatal.mg<sup>-1</sup> proteins. The protein content of the aliquots tested was determined by the Bradford method (Bradford, *Anal. Biochem.* 72, 248-254, 1976).

### **Example 11: *in vitro* conversion of linoleic acid by the T1 transgenic plants**

The level of LOX activity of the transgenic plants was compared with that of the parental lines 46-8 WT and 49-10 WT by measuring, *in vitro*, the ability of various enzyme extracts to convert a natural substrate of this enzyme, linoleic acid. These extracts, prepared from the aerial parts of 8-week-old plants, were incubated *in vitro* with  $^{14}\text{C}$ -labeled linoleic acid. The radiolabeled products, extracted and then separated by thin layer chromatography (TLC), were revealed using a phosphorimager. From the digitized TLC image, the linoleic

acid not metabolized at the end of the reaction was quantified for each lane and expressed as percentage of the linoleic acid measured in a control reaction not containing any enzyme extract. These percentages correspond to the mean of three independent repetitions. In the assays, the linoleic acid disappears almost completely in the lanes corresponding to the

5 transgenic plants S46-26 and S49-18 with only 5 and 10% of substrate remaining at the end of the reaction, whereas, in the case of the parental lines 46-8 WT and 49-10 WT, approximately 50% of the substrate is not metabolized. In order to verify that this difference between the WT and transgenic lines is indeed due to the constitutive expression of the transgene introduced, the same reaction was carried out by preincubating the enzyme

10 extracts with ETYA (5,8,11,14-eicosatetraynoic acid), a LOX-specific inhibitor. In this case, approximately 50% of the linoleic acid is detected at the end of the reaction both for the parental lines and for the transgenic lines. This suggests that all the lines have a LOX-independent activity capable of metabolizing part of the fatty acid introduced. When the enzyme extracts are boiled before being incubated with the substrate, between 80 and 90%

15 of the fatty acid is extracted at the end of the reaction, showing that an enzyme reaction is indeed involved and suggesting either that part of the substrate (between 10 and 20%) is chemically degraded, or that it is not extractable under the conditions used. This experiment therefore shows that the transgenic lines S46-26 and S49-18 exhibit ETYA-sensitive linoleic acid-converting activity, which is not the case of the parental lines 46-8 WT and 49-10 WT.

20 This shows that constitutive expression of the *LOX1* transgene, and also the presence of the LOX1 protein in the transgenic lines, also results in an increase in LOX activity in these plants. This increase in activity was also measured in the S46-21 line.

#### **Example 12: Inoculation of tobacco plants with *Ppn***

25 A method of stem inoculation of tobacco with *Ppn* was used. 12-week-old wild-type (46-8 WT and 49-10 WT lines) or transgenic tobacco plants were inoculated by application of a disc of mycelium onto the stem after sectioning of the apical part thereof (approximately a third of the way from the top) with a razor blade. The discs of mycelium originated from 7-day-old cultures in agar medium. Control plants were treated identically,

30 with the exception of the application of the mycelium disc, replaced with a disc of sterile medium. The control and inoculated stems were covered with an aluminum film so as to preserve the plant tissues and the mycelium against desiccation.

### **Example 13: Observation and measurement of symptoms**

The symptoms were observed and quantified 48 hours or 72 hours after inoculation. The stems were sectioned longitudinally and the length of the lesions was measured for each half-stem at five equidistant points, distributed over the entire width of the section. The  
 5 lesion length used for each individual corresponds to the mean of these 10 measurements.

### **Example 14: Measurement of *LOX1* transcript accumulation and of LOX specific activity in the stems of the T1 transgenic lines**

The method selected for testing the interaction between tobacco and the pathogenic  
 10 microorganism *Ppn* consists in inoculating the stem with *Ppn* mycelium, after sectioning the apex of the plant. As a prelude to this experiment, the level of expression of the transgene and also the LOX specific activity in the stems of the transgenic lines S46-21, S46-26 and S49-18 were compared with those observed in the parental lines 46-8 WT and 49-10 WT. For each line, total RNAs were prepared from a pool of 3 pieces of stem each originating  
 15 from an independent plant. The result of hybridization with a radiolabeled *LOX1* probe confirms LOX transcript accumulation in the stems of the transgenic lines S46-21, S46-26 and S49-18, whereas no LOX transcript is detected in the parental lines 46-8 WT and 49-10 WT. The LOX specific activity was also measured in this organ, using concentrated and dialyzed enzyme extracts. The analysis was carried out in a spectrophotometer by  
 20 measuring the appearance of fatty acid hydroperoxides at 234 nm. For each line studied, 3 independent measurements were taken. The results obtained, pooled in a histogram (Fig. 2), indicate that the LOX specific activity measured in the transgenic lines S46-21, S46-26 and S49-18 is 1.8 to 5 times greater than the level of activity measured in the parental lines 46-8 WT and 49-10 WT. In addition, these levels of activity reach 25% (S46-21) and 70%  
 25 (S49-18) of the level of LOX activity measured in tobacco cells elicited for 24 hours (353.8 nkat.mg<sup>-1</sup> protein, data not shown). This analysis therefore confirms that the constitutive expression of the LOX transgene, and also the increase in LOX activity, measured in the transgenic plants also characterizes the stems.

### **Example 15: Analysis of the interaction between *Ppn* and the T1 transgenic lines having constitutive LOX activity**

In order to examine the consequences of constitutive *LOX1* expression in the transgenic lines S46-21, S46-26 and S49-18 on their interaction with *Ppn*, 12-week-old plants of these lines were inoculated with this pathogenic agent at the level of the stems. The

symptoms obtained after inoculation with a virulent race of *Ppn* were compared with those observed during a compatible interaction involving the corresponding parental line. Thus, the lines S46-21, S46-26 and 46-8 WT were inoculated with race 1 of *Ppn*, whereas the lines S49-18 and 49-10 WT were inoculated with race 0 of *Ppn*. An incompatibility control  
 5 was carried out by inoculating the line 46-8 WT with race 0 of *Ppn*. The symptoms obtained 48 hours or 72 hours after inoculation were observed on longitudinal sections of the stems and the lesions were measured (Figure 3).

The symptoms observed on the parental lines 46-8 WT and 49-10 WT are typical of tobacco/*Ppn* interactions; the line 46-8 WT, inoculated with race 0 of *Ppn*, exhibits dry and  
 10 localized lesions characteristic of an incompatible interaction. On the other hand, the long brown macerated lesions observed in the 46-8 WT/*Ppn* 1 and 49-10 WT/*Ppn* 0 interactions reflect the colonization of the stem by the pathogenic agent and are typical of compatible interactions. In comparison with the latter, the lesions measured in the transgenic lines, inoculated with the same virulent race as that used with the corresponding parental line, are  
 15 clearly reduced. In the two transgenic lines selected, S46-21 and S46-26, inoculation with race 1 of the fungus does not cause the formation of these long macerated lesions. Lesions are observed which are much more reduced than in the compatible case, but also much less macerated. This difference is also observed when the compatible interaction 49-10 WT/*Ppn* 0 (*Ppn* 0-sensitive wild-type line) and the interaction between the transgenic line S49-18,  
 20 which is derived from the line 49-10 WT, and *Ppn* 0 are compared. It is observed that the lesions caused during the S46-26/*Ppn* 1 interaction resemble more closely the necroses which appear during an incompatible interaction (46-8 WT/*Ppn* 0) than the lesions which accompany the colonization of the plant tissues by the fungus in the case of a compatible interaction (46-8 WT/*Ppn* 1). For example, the lesions obtained 48 hours after inoculation in  
 25 the S46-21/*Ppn* 1 and S46-26/*Ppn* 1 interactions are respectively 3.4 and 2.4 times shorter than those measured in the compatible interaction 46-8 WT/*Ppn* 1. For the S49-18 line, inoculation with race 0 of *Ppn* causes lesions twice as short as those observed for the parental line 49-10 WT inoculated with the same race of the fungus. All these results show that constitutive LOX expression in the transgenic lines is accompanied by a clear limitation  
 30 of the progression of the fungus.

Besides the reduction in size of the lesions observed in the transgenic lines inoculated with a virulent race of *Ppn*, the nature thereof is also modified. The lesions obtained in the S46-26/*Ppn* 1 interaction are not macerated as in the compatible interaction 46-8 WT/*Ppn* 1, but are rather dry as in the incompatible interaction 46-8 WT/*Ppn* 0. This



shows that the constitutive LOX activity measured in the transgenic lines S46-21, S46-26 and S49-18 actively contribute to the resistance of tobacco to *Ppn*.

**Example 16: Analysis of the interaction between Ppn and the T1 transgenic plants**

**5 having constitutive LOX activity – root inoculation**

Plants constitutively expressing tobacco LOX1 were previously obtained. In a stem inoculation test, the plants showed reduced sensitivity to *Phytophthora parasitica* var. *nicotianae* (*Ppn*) in comparison with the wild-type line from which they are derived. The behavior of these plants was studied in a **root inoculation** test.

10 Wild-type tobacco plants (*Nicotiana tabacum* L.) of the 46-8 line (46-8 WT), characterized by the presence of a locus for resistance to race 0 of *Ppn*, and plants of the sense-lipoxygenase S46-21 transgenic line, derived from the 46-8 WT line, were sown *in vitro*. The seeds of wild-type or transgenic lines were sterilized and sown in Petri dishes, on solid MS medium at a rate of approximately 30 seeds per dish, by intercollating a disc of  
15 synthetic cloth between the medium and the seeds. The dishes were placed in a sloping position so as to orient the growth of the roots. After 3 weeks of growth *in vitro* (40% hygrometry, constant temperature 25°C, light 60  $\mu\text{mol.m}^{-2}.\text{s}^{-1}$ : 16h, dark: 8h), the discs of cloth supporting the plants were transferred into new Petri dishes containing liquid MS medium and glass beads, and the plants were returned to the culture chamber for 2 days,  
20 before inoculation. The *Ppn* strains used correspond to isolates 1156 (race 0) and 1452 (race 1). The *Ppn* mycelium was grown in the dark on a solid synthetic medium.

A method for root inoculation of tobacco using a suspension of *Ppn* zoospores was used. A *Ppn* mycelium colony obtained on V8 medium was placed under conditions of deficiency on agar-water for 4 days, and the zoospores were then released by cold shock  
25 (30 min at 15°C and then 30 min at ambient temperature) in 10 ml of water. After counting, the zoospore suspension is adjusted to 4000 spores/ml. For each dish, the liquid MS medium is removed and replaced with the spore suspension. The plants exhibiting no symptoms of disease are counted after 6 to 11 days, and the percentage survival (plants free of symptoms/total plants) is calculated for each combination.

30 In order to examine the consequences of constitutive *LOX1* expression in tobacco on the interaction with *Ppn*, 3-week-old plants of the S46-21 transgenic line were inoculated at the level of the roots with virulent race 1 of this pathogenic antigen. The outcome of the inoculated plants was compared with that of wild-type plants of the corresponding parental line 46-8 WT, inoculated with this same race (compatible interaction). An incompatibility

control was carried out, by inoculating the 46-8 WT line with race 0 of *Ppn* under the same conditions, as was a noninoculated control. The plants were observed 6 or 11 days after inoculation in a first experiment, and 7 days after inoculation in a second experiment. The plants free of symptoms of disease were counted and the percentage survivals were calculated (Table 1).

The 46-8 WT line inoculated with race 0 of *Ppn* exhibits no symptoms and the percentage survival is very close to 100%. On the other hand, in the 46-8 WT/*Ppn* 1 interaction, the colonization of the plants by the pathogenic antigen results in considerable mortality and a low percentage survival (20 to 24%). In comparison with this compatible interaction, the plants of the sense LOX S46-21 transgenic line, inoculated with the same virulent race as that used with the 46-8 WT line of origin, exhibit a much higher percentage survival, in two independent experiments (survival rate 80 to 88%). All these results confirm that constitutive LOX expression tobacco is accompanied by a notable reduction in sensitivity to *Ppn*.

**Table 1.** Percentage survival of the wild-type or sense-LOX transgenic plants, after inoculation with virulent race 1 of *Ppn*, and comparison with the incompatible interaction 46-8 WT/race 0

EXPERIMENT N° 1	Total	Survival rate <sup>a</sup>	
	number of plants	D6	D11
46-8 WT / <i>Ppn</i> 0 ( <b>incompatible</b> )	n=58	100%	100%
46-8 WT / <i>Ppn</i> 1 ( <b>compatible</b> )	n=55	24.0%	20.0%
<b>S46-21</b> / <i>Ppn</i> 1	n=54	88.8%	88.8%
EXPERIMENT N° 2		D7	
46-8 WT <b>control</b>	n=47	95.7%	
46-8 WT / <i>Ppn</i> 1 ( <b>compatible</b> )	n=82	21.9%	
<b>S46-21</b> / <i>Ppn</i> 1	n=65	80.0%	

<sup>a</sup> Survival rate = % number of plants without symptoms of disease/total number of plants.

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**Claims**

- 1) A method for reducing plant sensitivity to diseases and attacks from pathogenic  
5 organisms, characterized in that it consists in overexpressing a lipoxygenase in said plants.
- 2) The method as claimed in claim 1, characterized in that it consists in constitutively overexpressing a lipoxygenase in said plants.
- 10 3) The method as claimed in either of claims 1 and 2, in which said lipoxygenase has 9-lipoxygenase activity.
- 4) The method as claimed in one of claims 1 to 3, in which said lipoxygenase is a plant  
15 lipoxygenase.
- 5) The method as claimed in one of claims 1 to 4, in which said lipoxygenase is a Solanacea plant lipoxygenase.
- 20 6) The method as claimed in one of claims 1 to 5, in which said lipoxygenase is at least 80% homologous to the lipoxygenase of SEQ ID No. 1.
- 7) The method as claimed in claim 6, in which said lipoxygenase is represented in SEQ ID  
25 No. 1.
- 8) The method as claimed in one of claims 1 to 7, in which said lipoxygenase is overexpressed by integration into the genome of said plant of an expression cassette comprising a sequence encoding said lipoxygenase under the control of a promoter which is functional in plants.
- 30 9) The method as claimed in claim 8, in which said promoter is a promoter which is constitutive in plants.



- 10) The method as claimed in claim 9, in which said constitutive promoter is the cauliflower mosaic virus 35S promoter.
- 11) The method as claimed in one of claims 1 to 10, in which said lipoxygenase is  
5 overexpressed in the stems, the leaves and the roots of said plants.
- 12) An expression cassette which is functional in plant cells and plants, characterized in that it comprises a promoter having constitutive activity in plants, controlling the expression of a polynucleotide encoding a lipoxygenase at least 90% homologous to lipoxygenase  
10 of SEQ ID No. 1.
- 13) The expression cassette as claimed in claim 12, in which said polynucleotide encodes a lipoxygenase having 9-lipoxygenase activity.
- 15 14) The expression cassette as claimed in either of claims 12 and 13, in which said polynucleotide encodes the lipoxygenase of SEQ ID No. 1.
- 15) The expression cassette as claimed in one of claims 12 to 14, in which said promoter is the cauliflower mosaic virus 35S promoter.  
20
- 16) A vector, characterized in that it comprises an expression cassette as claimed in one of claims 12 to 15.
- 17) A transformed plant cell, characterized in that it comprises an expression cassette as  
25 claimed in one of claims 12 to 15 and/or a vector as claimed in claim 16.
- 18) A transformed plant, characterized in that it comprises an expression cassette as claimed in one of claims 12 to 15, a vector as claimed in claim 16 and/or transformed plant cells as claimed in claim 17.

**Abstract**

- 5        The present invention relates to methods for reducing plant sensitivity to diseases and attacks from pathogenic organisms. The methods according to the invention consist in overexpressing an inducible lipoxygenase in plants in order to improve their response to diseases and pathogens. The invention also relates to expression cassettes for overexpressing lipoxygenases in plants, and also to transformed plants.

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acc aaa aca gat cct aat tcc gag agc agg att cca ttg ctt atg agc	1307
Thr Lys Thr Asp Pro Asn Ser Glu Ser Arg Ile Pro Leu Leu Met Ser	
240 245 250 255	
tta gac ata tat gtg cca agg gac gag cga ttt ggt cat ata aag ttg	1355
Leu Asp Ile Tyr Val Pro Arg Asp Glu Arg Phe Gly His Ile Lys Leu	
260 265 270	
tca gac ttc ttg aca ttt gct ttg aaa tcc att gtg cag ttg ctt ctc	1403
Ser Asp Phe Leu Thr Phe Ala Leu Lys Ser Ile Val Gln Leu Leu Leu	
275 280 285	
cct gag ttt aag gct ttg ttc gat agc acg cat aat gag ttt gat agt	1451
Pro Glu Phe Lys Ala Leu Phe Asp Ser Thr His Asn Glu Phe Asp Ser	
290 295 300	
ttt gag gat gta ctt aaa ctg tat gaa gga gga atc aag ttg cct caa	1499
Phe Glu Asp Val Leu Lys Leu Tyr Glu Gly Gly Ile Lys Leu Pro Gln	
305 310 315	
ggc cct ttg ttg aaa gcc att act gat agc att cct tta gag ata cta	1547
Gly Pro Leu Leu Lys Ala Ile Thr Asp Ser Ile Pro Leu Glu Ile Leu	

320	325	330	335	
aaa gaa ctc ctt cga agt gat ggt gaa ggc cta ttt aag tac cca act Lys Glu Leu Leu Arg Ser Asp Gly Glu Gly Leu Phe Lys Tyr Pro Thr	340	345	350	1595
cct cag gtt att caa gag gat aaa act gca tgg agg acg gat gaa gaa Pro Gln Val Ile Gln Glu Asp Lys Thr Ala Trp Arg Thr Asp Glu Glu	355	360	365	1643
ttt ggg aga gaa atg ttg gcg gga gtc aat cct gtc ata atc agt aga Phe Gly Arg Glu Met Leu Ala Gly Val Asn Pro Val Ile Ile Ser Arg	370	375	380	1691
ctc caa gaa ttc cct ccg aaa agc aag ttg gat cct aaa ata tat ggc Leu Gln Glu Phe Pro Pro Lys Ser Lys Leu Asp Pro Lys Ile Tyr Gly	385	390	395	1739
aac caa aac agt aca att acc aga gag cag ata gag gat aag ttg gat Asn Gln Asn Ser Thr Ile Thr Arg Glu Gln Ile Glu Asp Lys Leu Asp	400	405	410	1787
gga cta aca att gat gag gca atc aag act aac aga cta ttc ata ttg Gly Leu Thr Ile Asp Glu Ala Ile Lys Thr Asn Arg Leu Phe Ile Leu	420	425	430	1835
aac cat cat gat atc ctt atg cca tac ttg agg aga att aac acg tcg Asn His His Asp Ile Leu Met Pro Tyr Leu Arg Arg Ile Asn Thr Ser	435	440	445	1883
aca gac aca aaa acc tat gcc tca aga act ctg ctc ttc ttg caa gat Thr Asp Thr Lys Thr Tyr Ala Ser Arg Thr Leu Leu Phe Leu Gln Asp	450	455	460	1931
aat gga act ttg aag cca tca gca att gaa cta agc ttg cca cat cca Asn Gly Thr Leu Lys Pro Ser Ala Ile Glu Leu Ser Leu Pro His Pro	465	470	475	1979
gac gga gat caa ttt ggc gct gtt agc aaa gta tat aca cca gct gat Asp Gly Asp Gln Phe Gly Ala Val Ser Lys Val Tyr Thr Pro Ala Asp	480	485	490	2027
caa ggt gtt gaa ggt tct atc tgg cag ttg gcc aaa gcc tat gca gca Gln Gly Val Glu Gly Ser Ile Trp Gln Leu Ala Lys Ala Tyr Ala Ala	500	505	510	2075
gtg aat gat tcg ggc gtt cat caa ctc atc agt cac tgg ttg aat aca Val Asn Asp Ser Gly Val His Gln Leu Ile Ser His Trp Leu Asn Thr	515	520	525	2123
cat gca gcg ata gag cca ttc gtg atc gca aca aat agg caa cta agc His Ala Ala Ile Glu Pro Phe Val Ile Ala Thr Asn Arg Gln Leu Ser	530	535	540	2171
gcg ctt cac cct att tat aag ctt ctc cac cct cat ttc cgt gag acg Ala Leu His Pro Ile Tyr Lys Leu Leu His Pro His Phe Arg Glu Thr	545	550	555	2219
atg aac ata aat gct tta gca aga cag atc ttg atc aac ggt ggt gga Met Asn Ile Asn Ala Leu Ala Arg Gln Ile Leu Ile Asn Gly Gly Gly	560	565	570	2267
ctt ctt gag ttg aca gtt ttt ccg gcc aaa tat tcc atg gaa atg tca				2315



Leu	Leu	Glu	Leu	Thr	Val	Phe	Pro	Ala	Lys	Tyr	Ser	Met	Glu	Met	Ser		
				580					585					590			
gca	gta	gtt	tac	aaa	gac	tgg	gtt	ttc	cct	gaa	caa	gca	ctt	cct	act	2363	
Ala	Val	Val	Tyr	Lys	Asp	Trp	Val	Phe	Pro	Glu	Gln	Ala	Leu	Pro	Thr		
			595					600					605				
gat	ctc	atc	aaa	aga	gga	gta	gct	gtt	gag	gac	tcg	agc	tcc	cca	ctt	2411	
Asp	Leu	Ile	Lys	Arg	Gly	Val	Ala	Val	Glu	Asp	Ser	Ser	Ser	Pro	Leu		
		610					615					620					
ggc	att	cga	tta	ctg	att	cag	gac	tat	cca	tat	gct	gtt	gat	ggg	ttg	2459	
Gly	Ile	Arg	Leu	Leu	Ile	Gln	Asp	Tyr	Pro	Tyr	Ala	Val	Asp	Gly	Leu		
	625					630					635						
aaa	att	tgg	tca	gca	att	aaa	agt	tgg	gta	act	gaa	tac	tgc	aac	tac	2507	
Lys	Ile	Trp	Ser	Ala	Ile	Lys	Ser	Trp	Val	Thr	Glu	Tyr	Cys	Asn	Tyr		
640					645					650					655		
tat	tac	aaa	tca	gat	gat	gcg	gtt	caa	aaa	gac	act	gaa	ctc	caa	gcc	2555	
Tyr	Tyr	Lys	Ser	Asp	Asp	Ala	Val	Gln	Lys	Asp	Thr	Glu	Leu	Gln	Ala		
				660					665					670			
tgg	tgg	aag	gaa	ctc	cgc	gaa	gag	gga	cac	ggc	gac	aag	aaa	gat	gag	2603	
Trp	Trp	Lys	Glu	Leu	Arg	Glu	Glu	Gly	His	Gly	Asp	Lys	Lys	Asp	Glu		
			675					680					685				
cct	tgg	tgg	cct	aaa	atg	cag	aca	gtg	caa	gaa	ttg	ata	gac	tct	tgc	2651	
Pro	Trp	Trp	Pro	Lys	Met	Gln	Thr	Val	Gln	Glu	Leu	Ile	Asp	Ser	Cys		
		690					695					700					
acc	atc	aca	ata	tgg	ata	gct	tca	gca	ctt	cat	gca	gca	gtc	aat	ttc	2699	
Thr	Ile	Thr	Ile	Trp	Ile	Ala	Ser	Ala	Leu	His	Ala	Ala	Val	Asn	Phe		
	705					710					715						
ggg	caa	tac	cct	tat	gct	ggc	tat	ctc	cct	aat	cgc	cct	aca	tta	agc	2747	
Gly	Gln	Tyr	Pro	Tyr	Ala	Gly	Tyr	Leu	Pro	Asn	Arg	Pro	Thr	Leu	Ser		
720					725					730					735		
cga	aat	ttc	atg	cca	gag	cca	gga	agt	cct	gag	tat	gaa	gag	ctc	aag	2795	
Arg	Asn	Phe	Met	Pro	Glu	Pro	Gly	Ser	Pro	Glu	Tyr	Glu	Glu	Leu	Lys		
				740					745					750			
aca	aat	ccg	gat	aag	gta	ttc	ctc	aaa	aca	atc	act	cct	cag	ctg	cag	2843	
Thr	Asn	Pro	Asp	Lys	Val	Phe	Leu	Lys	Thr	Ile	Thr	Pro	Gln	Leu	Gln		
			755					760					765				
aca	ctg	ctt	ggc	att	tcc	ctc	ata	gag	atc	ttg	tca	agg	cat	tct	tcg	2891	
Thr	Leu	Leu	Gly	Ile	Ser	Leu	Ile	Glu	Ile	Leu	Ser	Arg	His	Ser	Ser		
		770					775					780					
gat	aca	ctt	tac	ctc	ggg	caa	agg	gaa	tca	cct	gaa	tgg	aca	aag	gat	2939	
Asp	Thr	Leu	Tyr	Leu	Gly	Gln	Arg	Glu	Ser	Pro	Glu	Trp	Thr	Lys	Asp		
	785					790					795						
caa	gaa	cca	ctt	tca	gct	ttt	gcg	agg	ttt	gga	aag	aag	ctg	agt	gat	2987	
Gln	Glu	Pro	Leu	Ser	Ala	Phe	Ala	Arg	Phe	Gly	Lys	Lys	Leu	Ser	Asp		
800					805					810					815		
atc	gag	gat	cag	att	atg	cag	atg	aat	gtc	gat	gag	aaa	tgg	aag	aac	3035	
Ile	Glu	Asp	Gln	Ile	Met	Gln	Met	Asn	Val	Asp	Glu	Lys	Trp	Lys	Asn		
			820						825						830		

agg tcg ggt cct gtt aaa gtt cca tac acc ttg ctc ttc ccc aca agt 3083  
 Arg Ser Gly Pro Val Lys Val Pro Tyr Thr Leu Leu Phe Pro Thr Ser  
                   835                                  840                                  845

gaa gga gga ctt act ggc aaa gga att cct aac agt gtg tca ata tag 3131  
 Glu Gly Gly Leu Thr Gly Lys Gly Ile Pro Asn Ser Val Ser Ile  
                   850                                  855                                  860

aactttcccg atctagtaac atagatgaca ccgcgcgcga taatttatcc tagtttgcg 3191  
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